	38	52.8	10.1	129149	46	HS510D11	Z98044	Human DNA s
c	39	52.8	10.1	137143	55	AC068496	AC068496	Mus muscu
c	40	52.6	10.0	175280	49	AC023327	AC023327	Homo sapi
c	41	52.6	10.0	177568	46	HS388M5	Z97055	Human DNA s
c	42	52.6	10.0	206051	50	AC024914	AC024914	Mus muscu
c	43	52.2	10.0	153147	46	HS13D10	AL021407	Homo sapi
	44	52.2	10.0	155344	64	AL161899	AL161899	Homo sapi
c	45	52.2	10.0	170356	88	AF259072	AF259072	Mus muscu

ALIGNMENTS

RESULT   1
CVU20341
LOCUS   CVU20341   8158 bp   DNA   circular   VRL   25-OCT-1995
DEFINITION   Cassava vein mosaic virus, complete genome.
ACCESSION   U20341
VERSION   U20341.1 GI:665931
KEYWORDS   .
SOURCE   Cassava vein mosaic virus.
  ORGANISM   Cassava vein mosaic virus
             Viruses; Retroid viruses.
REFERENCE   1 (bases 1 to 8158)
  AUTHORS   Calvert,L.A., Ospina,M.D. and Shepherd,R.J.
  TITLE   Characterization of cassava vein mosaic virus: a distinct plant
             pararetrovirus
  JOURNAL   J. Gen. Virol. 76 (Pt 5), 1271-1278 (1995)
  MEDLINE   95248298
REFERENCE   2 (bases 1 to 8158)
  AUTHORS   Calvert,L.A.
  TITLE   Direct Submission
  JOURNAL   Submitted (26-JAN-1995) Lee A. Calvert, Virology Unit, Centro
             Internacional de Agricultura Tropical, A.A. 6713, Cali, Valle,
             Colombia
FEATURES   Location/Qualifiers
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     CDS   30. .4148
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                     /db_xref="GI:665932"
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                     NLADRINYLQNINTSIDFKLWKMNKENLERQELLLRQINELKEEIKSLKNIPSTVAII
                     PTNTYTINMIRTETEDWKYFKYIEKELVQNKTEAIAKILDNSYIINDNLGLLYERYEE
                     INPTPKPYKRPETIFDTPQYAKYIRNQKRQEEYEKQQELKKENENKEYQEFLEWKEKQ
                     QKDKGKGIQTVYPTLIIPDIKPEKQKKEDMMLEMIKNLQNELEQLKIQRHKEHEKQAE
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                     QFIRRTFIGNVKEWYKNLTNEAKQKLEGNAPLLSLTHMELGLRAEFGKLGIESDVEKH
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93:    gb_vi1:*
94:    gb_vi2:*
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Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

	Result No.	Score	% Query Match	Length	DB	ID	Description
	1	514.6	98.2	8158	93	CVU20341	U20341 Cassava vei
	2	514.6	98.2	8159	93	CVU59751	U59751 Cassava vei
c	3	77	14.7	7218	5	I66494	I66494 Sequence 14
	4	60.4	11.5	112585	46	HS1059E7	AL023095 Human DNA
	5	59	11.3	276598	37	AC012382	AC012382 Mus muscu
	6	58.4	11.1	193432	57	AC073290	AC073290 Mus muscu
	7	58.2	11.1	259421	57	AC073689	AC073689 Mus muscu
c	8	58	11.1	171743	53	AC055806	AC055806 Homo sapi
	9	57.6	11.0	204985	57	AC073938	AC073938 Mus muscu
c	10	57.6	11.0	237908	47	AC020971	AC020971 Mus muscu
	11	57	10.9	163229	10	AC009039	AC009039 Homo sapi
	12	56.8	10.8	211308	57	AC073613	AC073613 Homo sapi
	13	56.2	10.7	513	88	RNU83985	U83985 Rattus norv
	14	56.2	10.7	60058	48	AC022549	AC022549 Mus muscu
	15	56.2	10.7	147266	10	AC005913	AC005913 Homo sapi
	16	56.2	10.7	159818	27	AC007337	AC007337 Homo sapi
	17	56.2	10.7	204318	88	AC026387	AC026387 Mus muscu
c	18	55.6	10.6	115976	57	AC073502	AC073502 Homo sapi
c	19	55.6	10.6	153664	53	AC040971	AC040971 Homo sapi
c	20	55.2	10.5	136037	9	AC004104	AC004104 Homo sapi
c	21	55	10.5	161996	63	AL133401	AL133401 Mus muscu
	22	55	10.5	181636	50	AC025108	AC025108 Homo sapi
	23	55	10.5	194615	36	AC010184	AC010184 Homo sapi
c	24	55	10.5	200275	57	AC073883	AC073883 Mus muscu
	25	54.6	10.4	71618	7	AB012240	AB012240 Arabidops
	26	54.6	10.4	200573	49	AC024116	AC024116 Mus muscu
c	27	54.4	10.4	212042	57	AC073904	AC073904 Homo sapi
	28	54.2	10.3	147156	56	AC068998	AC068998 Mus muscu
c	29	54	10.3	35875	35	AP000454	AP000454 Homo sapi
c	30	54	10.3	91748	88	AF177767	AF177767 Mus muscu
c	31	54	10.3	169328	35	AP000472	AP000472 Homo sapi
	32	54	10.3	183330	38	AC015932	AC015932 Mus muscu
c	33	54	10.3	340000	35	AP001683	AP001683 Homo sapi
	34	53.4	10.2	131169	84	AL356779	AL356779 Homo sapi
c	35	53.4	10.2	165313	84	AL356742	AL356742 Homo sapi
	36	53	10.1	53889	8	F14O10	AC026234 Sequence
	37	53	10.1	221285	49	AC023611	AC023611 Mus muscu

GenCore version 4.5
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OM nucleic - nucleic search, using sw model

Run on: December 17, 2000, 01:31:17 ; Search time 990.18 Seconds
                                              (without alignments)
                                              2311.309 Million cell updates/sec

Title: US-09-202-838-3
Perfect score: 524
Sequence: 1 ggtaccagaaggtaattatc..........aaatttgtaagtttgaattc 524

Scoring table: IDENTITY_NUC
                 Gapop 10.0 , Gapext 1.0

Searched: 1033670 seqs, 2183789903 residues

Total number of hits satisfying chosen parameters: 2067340

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
                 Maximum Match 100%
                 Listing first 45 summaries

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